



#6

SEQUENCE LISTING

SEQUENCING LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<111> THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES

<130> 11217W03

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<150> H11-372826

<151> 1999-12-28

<150> PCT-JP00-01148

<151> 2000-02-28

<150> PCT-JP00-07741

<151> 2000-11-02

<160>80

<170> PatentIn Ver.2.0

<210> 1

<211> 411

<212> PRT

<213> Homo sapiens

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Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
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Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
35 40 45

Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335

Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365
 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
 370 375 380
 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
 385 390 395 400
 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
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<210> 2

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

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ggg gag agt gcg gcg ggc ggc agc ggc gct ggc ggc gac tcc gcc ata	96
Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile	
20 25 30	
gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc	144
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly	
35 40 45	
gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg	192
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp	
50 55 60	
aag cag gcg ggc cgg ggc ggc ggc gtc tgt ggc cgt ggc cgg ggc cgg	240
Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg	
65 70 75 80	
ggc cgt ggc cgg gga cgg gga cgg ggc cgg ggc cgg ggc cgc ggc cgt	288
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg	
85 90 95	

ccc ccg agt ggc ggc agc ggc ctt ggc ggc gac ggc ggc ggc tgc ggc	336
Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly	
100 105 110	
ggc ggc ggc agc ggt ggc ggc ggc gcc ccc cgg cgg gag ccg gtc cct	384
Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro	
115 120 125	
ttc ccg tcg ggg agc gcg ggg ccg ggg ccc agg gga ccc cgg gcc acg	432
Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr	
130 135 140	
gag agc ggg aag agg atg gat tgc ccg gcc ctc ccc ccc gga tgg aag	480
Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys	
145 150 155 160	
aag gag gaa gtg atc cga aaa tct ggg cta agt gct ggc aag agc gat	528
Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp	
165 170 175	
gtc tac tac ttc agt cca agt ggt aag aag ttc aga agc aag cct cag	576
Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln	
180 185 190	
ttg gca agg tac ctg gga aat act gtt gat ctc agc agt ttt gac ttc	624
Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe	
195 200 205	
aga act gga aag atg atg cct agt aaa tta cag aag aac aaa cag aga	672
Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg	
210 215 220	
ctg cga aac gat cct ctc aat caa aat aag ggt aaa cca gac ttg aat	720
Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn	
225 230 235 240	
aca aca ttg cca att aga caa aca gca tca att ttc aaa caa ccg gta	768
Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val	
245 250 255	
acc aaa gtc aca aat cat cct agt aat aaa gtg aaa tca gac cca caa	816
Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln	
260 265 270	
cga atg aat gaa cag cca cgt cag ctt ttc tgg gag aag agg cta caa	864
Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln	
275 280 285	

gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa	912
Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu	
290 295 300	
cta ccc aaa ggt ctt caa gga gtt ggt cca ggt agc aat gat gag acc	960
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr	
305 310 315 320	
ctt tta tct gct gtt gcc agt gct ttg cac aca agc tct gcg cca atc	1008
Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile	
325 330 335	
aca ggg caa gtc tcc gct gct gtg gaa aag aac cct gct gtt tgg ctt	1056
Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu	
340 345 350	
aac aca tct caa ccc ctc tgc aaa gct ttt att gtc aca gat gaa gac	1104
Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp	
355 360 365	
atc agg aaa cag gaa gag cga gta cag caa gta cgc aag aaa ttg gaa	1152
Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu	
370 375 380	
gaa gca ctg atg gca gac atc ttg tcg cga gct gct gat aca gaa gag	1200
Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu	
385 390 395 400	
atg gat att gaa atg gac agt gga gat gaa gcc	1233
Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala	
405 410	

<210> 3

<211> 196

<212> PRT

<213> Homo sapiens

<400> 3

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20 25 30
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
35 40 45
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg

50		55		60
Ala His Gly Val His	Ala Thr Lys His Val	Pro Glu Lys Arg Pro	Leu	
65	70	75	80	
Pro Ile Arg Arg Lys	Arg Ser Ile Glu Glu	Ala Val Pro Ala	Val Cys	
	85	90	95	
Lys Thr Arg Thr Val	Ile Tyr Glu Ile	Pro Arg Ser Gln	Val Asp Pro	
	100	105	110	
Thr Ser Ala Asn Phe	Leu Ile Trp Pro	Pro Cys Val Glu	Val Lys Arg	
	115	120	125	
Cys Thr Gly Cys Cys	Asn Thr Ser Ser	Val Lys Cys Gln	Pro Ser Arg	
	130	135	140	
Val His His Arg Ser	Val Lys Val Ala	Lys Val Glu Tyr	Val Arg Lys	
	145	150	155	160
Lys Pro Lys Leu Lys	Glu Val Gln Val	Arg Leu Glu Glu	His Leu Glu	
	165	170	175	
Cys Ala Cys Ala Thr	Thr Ser Leu Asn	Pro Asp Tyr Arg	Glu Glu Asp	
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Thr Asp Val Arg				
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<211> 588

<212> DNA

<213> Homo sapiens

<220>

<221> CDS.

<223> (1)..(591)

<400> 4

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1	5	10	15
cat gtt ctg gcc gag gaa	gcc gag atc ccc cgc	gag gtg atc gag agg	96
His Val Leu Ala Glu Glu	Ala Glu Ile Pro Arg	Glu Val Ile Glu Arg	
	20	25	30
ctg gcc cgc agt cag atc	cac agc atc cgg gac	ctc cag cga ctc ctg	144
Leu Ala Arg Ser Gln Ile	His Ser Ile Arg Asp	Leu Gln Arg Leu Leu	
	35	40	45

gag ata gac tcc gta ggg agt gag gat tct ttg gac acc agc ctg aga	192
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg	
50 55 60	
gct cac ggg gtc cac gcc act aag cat gtg ccc gag aag cgg ccc ctg	240
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu	
65 70 75 80	
ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc	288
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys	
85 90 95	
aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc	336
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro	
100 105 110	
acg tcc gcc aac ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc	384
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg	
115 120 125	
tgc acc ggc tgc tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc	432
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg	
130 135 140	
gtc cac cac cgc agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag	480
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys	
145 150 155 160	
aag cca aaa tta aaa gaa gtc cag gtg agg tta gag gag cat ttg gag	528
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu	
165 170 175	
tgc gcc tgc gcg acc aca agc ctg aat ccg gat tat cgg gaa gag gac	576
Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp	
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acg gat gtg agg	588
Thr Asp Val Arg	
195	
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<211> 241	
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Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu			
35	40	45	
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met			
50	55	60	
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg			
65	70	75	80
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu			
85	90	95	
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp			
100	105	110	
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln			
115	120	125	
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr			
130	135	140	
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg			
145	150	155	160
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu			
165	170	175	
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser			
180	185	190	
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val			
195	200	205	
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg			
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Ala			

<210> 6

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(726)

<400> 6

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ctg gtc agc gcc gag ggg gac ccc att ccc gag gag ctt tat gag atg	96
Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met	
20 25 30	
ctg agt gac cac tcg atc cgc tcc ttt gat gat ctc caa cgc ctg ctg	144
Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu	
35 40 45	
cac gga gac ccc gga gag gaa gat ggg gcc gag ttg gac ctg aac atg	192
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met	
50 55 60	
acc cgc tcc cac tct gga ggc gag ctg gag agc ttg gct cgt gga aga	240
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg	
65 70 75 80	
agg agc ctg ggt tcc ctg acc att gct gag ccg gcc atg atc gcc gag	288
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu	
85 90 95	
tgc aag acg cgc acc gag gtg ttc gag atc tcc cgg cgc ctc ata gac	336
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp	
100 105 110	
cgc acc aac gcc aac ttc ctg gtg tgg ccg ccc tgt gtg gag gtg cag	384
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln	
115 120 125	
cgc tgc tcc ggc tgc tgc aac aac cgc aac gtg cag tgc cgc ccc acc	432
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr	
130 135 140	
cag gtg cag ctg cga cct gtc cag gtg aga aag atc gag att gtg cgg	480
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg	
145 150 155 160	
aag aag cca atc ttt aag aag gcc acg gtg acg ctg gaa gac cac ctg	528
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu	
165 170 175	
gca tgc aag tgt gag aca gtg gca gct gca cgg cct gtg acc cga agc	576

Ala Cys Lys Cys Glu Thr Val	Ala Ala Ala Arg Pro Val Thr Arg Ser	
180	185	190
cgc ggg ggt tcc cag gag cag cga gcc aaa acg ccc caa act cgg gtg		624
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val		
195	200	205
acc att cgg acg gtg cga gtc cgc cgg ccc ccc aag ggc aag cac cgg		672
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg		
210	215	220
aaa ttc aag cac acg cat gac aag acg gca ctg aag gag acc ctt gga		720
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly		
225	230	235
		240
gcc		723
Ala		
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Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg		
35	40	45
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu		
50	55	60
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn		
65	70	75
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys		
85	90	95
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr		
100	105	110
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys		
115	120	125
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys		
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Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser

145

150

<210> 8

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(468)

<400> 8

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ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg	96
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu	
20 25 30	
tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga	144
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg	
35 40 45	
gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt	192
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu	
50 55 60	
caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac	240
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn	
65 70 75 80	
cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt	288
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys	
85 90 95	
gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac	336
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr	
100 105 110	
aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ttg aaa	384
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys	
115 120 125	
cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa	432
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys	

210	215	220
Arg Asp Gly Lys Pro Cys Leu Gly Asp Ser Ala Pro Tyr Ala Pro Ala		
225	230	235 240
Tyr Gly Val Gly Leu Asn Pro Tyr Gly Tyr Asn Ala Tyr Pro Ala Tyr		
245	250	255
Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala		
260	265	270
Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala		
275	280	285
Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln		
290	295	300
Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly		
305	310	315 320
Ile Arg Ala Trp		

<210> 10

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(975)

<400> 10

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Met Phe Pro Ser Pro Ala Leu Thr Pro Thr Pro Phe Ser Val Lys Asp	
1 5 10 15	
atc cta aac ctg gaa cag cag cag cgc agc ctg gct gcc gcc gga gag	96
Ile Leu Asn Leu Glu Gln Gln Gln Arg Ser Leu Ala Ala Ala Gly Glu	
20 25 30	
ctc tct gcc cgc ctg gag gcg acc ctg gcg ccc tcc tcc tgc atg ctg	144
Leu Ser Ala Arg Leu Glu Ala Thr Leu Ala Pro Ser Ser Cys Met Leu	
35 40 45	
gcc gcc ttc aag cca gag gcc tac gct ggg ccc gag gcg gct gcg ccg	192
Ala Ala Phe Lys Pro Glu Ala Tyr Ala Gly Pro Glu Ala Ala Ala Pro	
50 55 60	
ggc ctc cca gag ctg cgc gca gag ctg ggc cgc gcg cct tca ccg gcc	240

Gly	Leu	Pro	Glu	Leu	Arg	Ala	Glu	Leu	Gly	Arg	Ala	Pro	Ser	Pro	Ala		
65						70					75				80		
aag	tgt	gcg	tct	gcc	ttt	ccc	gcc	gcc	ccc	gcc	ttc	tat	cca	cgt	gcc	288	
Lys	Cys	Ala	Ser	Ala	Phe	Pro	Ala	Ala	Pro	Ala	Phe	Tyr	Pro	Arg	Ala		
			85						90					95			
tac	agc	gac	ccc	gac	cca	gcc	aag	gac	cct	aga	gcc	gaa	aag	aaa	gag	336	
Tyr	Ser	Asp	Pro	Asp	Pro	Ala	Lys	Asp	Pro	Arg	Ala	Glu	Lys	Lys	Glu		
			100						105					110			
ctg	tgc	gcg	ctg	cag	aag	gcg	gtg	gag	ctg	gag	aag	aca	gag	gcg	gac	384	
Leu	Cys	Ala	Leu	Gln	Lys	Ala	Val	Glu	Leu	Glu	Lys	Thr	Glu	Ala	Asp		
			115					120					125				
aac	gcg	gag	cgg	ccc	cgg	gcg	cga	cgg	cgg	agg	aag	ccg	cgc	gtg	ctc	432	
Asn	Ala	Glu	Arg	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Lys	Pro	Arg	Val	Leu		
			130				135				140						
ttc	tcg	cag	gcg	cag	gtc	tat	gag	ctg	gag	cgg	cgc	ttc	aag	cag	cag	480	
Phe	Ser	Gln	Ala	Gln	Val	Tyr	Glu	Leu	Glu	Arg	Arg	Phe	Lys	Gln	Gln		
			145			150				155				160			
cgg	tac	ctg	tcg	gcc	ccc	gaa	cgc	gac	cag	ctg	gcc	agc	gtg	ctg	aaa	528	
Arg	Tyr	Leu	Ser	Ala	Pro	Glu	Arg	Asp	Gln	Leu	Ala	Ser	Val	Leu	Lys		
				165					170					175			
ctc	acg	tcc	acg	cag	gtc	aag	atc	tgg	ttc	cag	aac	cgg	cgc	tac	aag	576	
Leu	Thr	Ser	Thr	Gln	Val	Lys	Ile	Trp	Phe	Gln	Asn	Arg	Arg	Tyr	Lys		
				180				185				190					
tgc	aag	cgg	cag	cgg	cag	gac	cag	act	ctg	gag	ctg	gtg	ggg	ctg	ccc	624	
Cys	Lys	Arg	Gln	Arg	Gln	Asp	Gln	Thr	Leu	Glu	Leu	Val	Gly	Leu	Pro		
			195				200					205					
ccg	ccg	ccg	ccg	ccg	cct	gcc	cgc	agg	atc	gcg	gtg	cca	gtg	ctg	gtg	672	
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Arg	Arg	Ile	Ala	Val	Pro	Val	Leu	Val	
					210		215					220					
cgc	gat	ggc	aag	cca	tgc	cta	ggg	gac	tcg	gcg	ccc	tac	gcg	cct	gcc	720	
Arg	Asp	Gly	Lys	Pro	Cys	Leu	Gly	Asp	Ser	Ala	Pro	Tyr	Ala	Pro	Ala		
			225			230			235				240				
tac	ggc	gtg	ggc	ctc	aat	ccc	tac	ggt	tat	aac	gcc	tac	ccc	gcc	tat	768	
Tyr	Gly	Val	Gly	Leu	Asn	Pro	Tyr	Gly	Tyr	Asn	Ala	Tyr	Pro	Ala	Tyr		
				245				250					255				
ccg	ggt	tac	ggc	ggc	gcg	gcc	tgc	agc	cct	ggc	tac	agc	tgc	act	gcc	816	

Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala	
260	265 270
gct tac ccc gcc ggg cct tcc cca gcg cag ccg gcc act gcc gcc gcc	864
Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala	
275 280 285	
aac aac aac ttc gtg aac ttc ggc gtc ggg gac ttg aat gcg gtt cag	912
Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln	
290 295 300	
agc ccc ggg att ccg cag agc aac tcg gga gtg tcc acg ctg cat ggt	960
Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly	
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Ile Arg Ala Trp	
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35 40 45	
Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly	
50 55 60	
Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro	
65 70 75 80	
Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly	
85 90 95	
Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly	
100 105 110	
Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Arg Glu	
115 120 125	
Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala	

130	135	140
Gly Arg Glu Gln Tyr	Gly Arg Ala Gly Phe Ala Gly	Ser Tyr Ser Ser
145	150	155
Pro Tyr Pro Ala Tyr Met	Ala Asp Val Gly Ala Ser	Trp Ala Ala Ala
165	170	175
Ala Ala Ala Ser Ala Gly	Pro Phe Asp Ser Pro	Val Leu His Ser Leu
180	185	190
Pro Gly Arg Ala Asn Pro	Ala Ala Arg His Pro	Asn Leu Asp Met Phe
195	200	205
Asp Asp Phe Ser Glu Gly	Arg Glu Cys Val Asn	Cys Gly Ala Met Ser
210	215	220
Thr Pro Leu Trp Arg Arg	Asp Gly Thr Gly His	Tyr Leu Cys Asn Ala
225	230	235
Cys Gly Leu Tyr His Lys	Met Asn Gly Ile Asn	Arg Pro Leu Ile Lys
245	250	255
Pro Gln Arg Arg Leu Ser	Ala Ser Arg Arg Val	Gly Leu Ser Cys Ala
260	265	270
Asn Cys Gln Thr Thr Thr	Thr Thr Thr Leu Trp	Arg Arg Asn Ala Glu Gly
275	280	285
Glu Pro Val Cys Asn Ala	Cys Gly Leu Tyr Met	Lys Leu His Gly Val
290	295	300
Pro Arg Pro Leu Ala Met	Arg Lys Glu Gly Ile	Gln Thr Arg Lys Arg
305	310	315
Lys Pro Lys Asn Leu Asn	Lys Ser Lys Thr Pro	Ala Ala Pro Ser Gly
325	330	335
Ser Glu Ser Leu Pro Pro	Ala Ser Gly Ala Ser	Ser Ser Asn Ser Ser Asn
340	345	350
Ala Thr Thr Ser Ser Ser	Glu Glu Met Arg Pro	Ile Lys Thr Glu Pro
355	360	365
Gly Leu Ser Ser His Tyr	Gly His Ser Ser Ser	Val Ser Gln Thr Phe
370	375	380
Ser Val Ser Ala Met Ser	Gly His Gly Pro Ser	Ile His Pro Val Leu
385	390	395
Ser Ala Leu Lys Leu Ser	Pro Gln Gly Tyr Ala	Ser Pro Val Ser Gln
405	410	415
Ser Pro Gln Thr Ser Ser	Lys Gln Asp Ser Trp	Asn Ser Leu Val Leu

420 425 430
 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
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 Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala
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 gcg tcc tcg cca gtc tac ctg ccc aca ccg ccg gtg ccc tcc tcc gtt 144
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 ctg ggc ctg tcc tac ctc cag ggc gga ggc gcg ggc tct gcg tcc gga 192
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 ggc ccc tcg ggc ggc agc ccc ggt ggg gcc gcg tct ggt gcg ggg ccc 240
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 ggg acc cag cag ggc agc ccg gga tgg agc cag gcg gga gcg acc gga 288
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 gcc gct tac acc ccg ccg ccg gtg tcg ccg cgc ttc tcc ttc ccg ggg 336
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 acc acc ggg tcc ctg gcg gcg gcg gcg gcg gct gcc gcc gcc ccg gaa 384
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 gct gcg gcc tac agc agt ggc ggc gga gcg gcg ggt gcg ggc ctg gcg 432

Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala	
130	135 140
ggc cgc gag cag tac ggg cgc gcc ggc ttc gcg ggc tcc tac tcc agc	480
Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser	
145 150 155 160	
ccc tac ccg gct tac atg gcc gac gtg ggc gcg tcc tgg gcc gca gcc	528
Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala	
165 170 175	
gcc gcc gcc tcc gcc ggc ccc ttc gac agc ccg gtc ctg cac agc ctg	576
Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu	
180 185 190	
ccc ggc cgg gcc aac ccg gcc gcc cga cac ccc aat ctc gat atg ttt	624
Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe	
195 200 205	
gac gac ttc tca gaa ggc aga gag tgt gtc aac tgt ggg gct atg tcc	672
Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser	
210 215 220	
acc ccg ctc tgg agg cga gat ggg acg ggt cac tat ctg tgc aac gcc	720
Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala	
225 230 235 240	
tgt ggc ctc tac cac aag atg aac ggc atc aac ccg ccg ctc atc aag	768
Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys	
245 250 255	
cct cag cgc cgg ctg tcc gcc tcc cgc cga gtg ggc ctc tcc tgt gcc	816
Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala	
260 265 270	
aac tgc cag acc acc acc acc acc acg ctg tgg cgc cgc aat gcg gag ggc	864
Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly	
275 280 285	
gag cct gtg tgc aat gcc tgc ggc ctc tac atg aag ctc cac ggg gtg	912
Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val	
290 295 300	
ccc agg cct ctt gca atg cgg aaa gag ggg atc caa acc aga aaa cgg	960
Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg	
305 310 315 320	
aag ccc aag aac ctg aat aaa tct aag aca cca gca gct cct tca ggc	1008

Lys	Pro	Lys	Asn	Leu	Asn	Lys	Ser	Lys	Thr	Pro	Ala	Ala	Pro	Ser	Gly		
			325						330					335			
agt	gag	agc	ctt	cct	ccc	gcc	agc	ggt	gct	tcc	agc	aac	tcc	agc	aac	1056	
Ser	Glu	Ser	Leu	Pro	Pro	Ala	Ser	Gly	Ala	Ser	Ser	Asn	Ser	Ser	Asn		
			340					345					350				
gcc	acc	acc	agc	agc	agc	gag	gag	atg	cgt	ccc	atc	aag	acg	gag	cct	1104	
Ala	Thr	Thr	Ser	Ser	Ser	Glu	Glu	Met	Arg	Pro	Ile	Lys	Thr	Glu	Pro		
			355					360					365				
ggc	ctg	tca	tct	cac	tac	ggg	cac	agc	agc	tcc	gtg	tcc	cag	acg	ttc	1152	
Gly	Leu	Ser	Ser	His	Tyr	Gly	His	Ser	Ser	Ser	Val	Ser	Gln	Thr	Phe		
			370				375				380						
tca	gtc	agt	gcg	atg	tct	ggc	cat	ggg	ccc	tcc	atc	cac	cct	gtc	ctc	1200	
Ser	Val	Ser	Ala	Met	Ser	Gly	His	Gly	Pro	Ser	Ile	His	Pro	Val	Leu		
			385			390			395					400			
tcg	gcc	ctg	aag	ctc	tcc	cca	caa	ggc	tat	gcg	tct	ccc	gtc	agc	cag	1248	
Ser	Ala	Leu	Lys	Leu	Ser	Pro	Gln	Gly	Tyr	Ala	Ser	Pro	Val	Ser	Gln		
			405					410					415				
tct	cca	cag	acc	agc	tcc	aag	cag	gac	tct	tgg	aac	agt	ctg	gtc	ttg	1296	
Ser	Pro	Gln	Thr	Ser	Ser	Lys	Gln	Asp	Ser	Trp	Asn	Ser	Leu	Val	Leu		
			420					425					430				
gcc	gac	agt	cac	ggg	gac	ata	atc	act	gcg							1326	
Ala	Asp	Ser	His	Gly	Asp	Ile	Ile	Thr	Ala								
			435					440									

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Met	Gly	Arg	Lys	Lys	Ile	Gln	Ile	Thr	Arg	Ile	Met	Asp	Glu	Arg	Asn		
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Arg	Gln	Val	Thr	Phe	Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala		
			20					25					30				
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe		
		35					40					45					
Asn	Ser	Ser	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys		
	50					55					60						

Val	Leu	Leu	Lys	Tyr	Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr	65	70	75	80
Asn	Ser	Asp	Ile	Val	Glu	Ala	Leu	Asn	Lys	Lys	Glu	His	Arg	Gly	Cys	85	90	95	
Asp	Ser	Pro	Asp	Pro	Asp	Thr	Ser	Tyr	Val	Leu	Thr	Pro	His	Thr	Glu	100	105	110	
Glu	Lys	Tyr	Lys	Lys	Ile	Asn	Glu	Glu	Phe	Asp	Asn	Met	Met	Arg	Asn	115	120	125	
His	Lys	Ile	Ala	Pro	Gly	Leu	Pro	Pro	Gln	Asn	Phe	Ser	Met	Ser	Val	130	135	140	
Thr	Val	Pro	Val	Thr	Ser	Pro	Asn	Ala	Leu	Ser	Tyr	Thr	Asn	Pro	Gly	145	150	155	160
Ser	Ser	Leu	Val	Ser	Pro	Ser	Leu	Ala	Ala	Ser	Ser	Thr	Leu	Thr	Asp	165	170	175	
Ser	Ser	Met	Leu	Ser	Pro	Pro	Gln	Thr	Thr	Leu	His	Arg	Asn	Val	Ser	180	185	190	
Pro	Gly	Ala	Pro	Gln	Arg	Pro	Pro	Ser	Thr	Gly	Asn	Ala	Gly	Gly	Met	195	200	205	
Leu	Ser	Thr	Thr	Asp	Leu	Thr	Val	Pro	Asn	Gly	Ala	Gly	Ser	Ser	Pro	210	215	220	
Val	Gly	Asn	Gly	Phe	Val	Asn	Ser	Arg	Ala	Ser	Pro	Asn	Leu	Ile	Gly	225	230	235	240
Ala	Thr	Gly	Ala	Asn	Ser	Leu	Gly	Lys	Val	Met	Pro	Thr	Lys	Ser	Pro	245	250	255	
Pro	Pro	Pro	Gly	Gly	Gly	Asn	Leu	Gly	Met	Asn	Ser	Arg	Lys	Pro	Asp	260	265	270	
Leu	Arg	Val	Val	Ile	Pro	Pro	Ser	Ser	Lys	Gly	Met	Met	Pro	Pro	Leu	275	280	285	
Ser	Glu	Glu	Glu	Glu	Leu	Glu	Leu	Asn	Thr	Gln	Arg	Ile	Ser	Ser	Ser	290	295	300	
Gln	Ala	Thr	Gln	Pro	Leu	Ala	Thr	Pro	Val	Val	Ser	Val	Thr	Thr	Pro	305	310	315	320
Ser	Leu	Pro	Pro	Gln	Gly	Leu	Val	Tyr	Ser	Ala	Met	Pro	Thr	Ala	Tyr	325	330	335	
Asn	Thr	Asp	Tyr	Ser	Leu	Thr	Ser	Ala	Asp	Leu	Ser	Ala	Leu	Gln	Gly	340	345	350	

Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
 355 360 365
 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
 370 375 380
 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
 405 410 415
 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
 420 425 430
 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
 435 440 445
 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
 450 455 460
 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
 465 470 475 480
 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
 485 490 495
 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
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<211> 1521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1524)

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Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn	
1 5 10 15	
cga cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	

35	40	45	
aac agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa			192
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys			
50	55	60	
gtt ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc			288
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys			
85	90	95	
gac agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa			336
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu			
100	105	110	
gaa aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat			384
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn			
115	120	125	
cat aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc			432
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val			
130	135	140	
aca gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg			480
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly			
145	150	155	160
agt tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat			528
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp			
165	170	175	
tca agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct			576
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser			
180	185	190	
cct gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg			624
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met			
195	200	205	
ttg agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca			672
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro			
210	215	220	
gtg ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga			720
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly			

225	230	235	240	
gct act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc				768
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro				
245	250	255		
cct cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat				816
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp				
260	265	270		
ctt cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta				864
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu				
275	280	285		
tcg gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct				912
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser				
290	295	300		
caa gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca				960
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro				
305	310	315	320	
agc ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac				1008
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr				
325	330	335		
aac act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc				1056
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly				
340	345	350		
ttc aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag				1104
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln				
355	360	365		
cag cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg				1152
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly				
370	375	380		
cag tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc				1200
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile				
385	390	395	400	
agc atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca				1248
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro				
405	410	415		
tcg ggc ttc cag cag cag cag cag cag cag cag cag cag ccg ccg				1296
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro				

420	425	430	
cca cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag			1344
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln			
435	440	445	
gaa atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc			1392
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser			
450	455	460	
tat gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca			1440
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro			
465	470	475	480
att gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct			1488
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser			
485	490	495	
gta aag cga atg agg atg gac gcg tgg gtg acc			1521
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr			
500	505		

<210> 15

<211> 365

<212> PRT

<213> Homo sapiens

<400> 15

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe			
35	40	45	
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg			
50	55	60	
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr			
65	70	75	80
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp			
85	90	95	
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys			
100	105	110	
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro			

115	120	125
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr		
130	135	140
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala		
145	150	155
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys		
165	170	175
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu		
180	185	190
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg		
195	200	205
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr		
210	215	220
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr		
225	230	235
Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro		
245	250	255
Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro		
260	265	270
Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg		
275	280	285
Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys		
290	295	300
Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys		
305	310	315
Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly		
325	330	335
Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp		
340	345	350
Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln		
355	360	

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<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1098)

<400> 16

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Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn	
1 5 10 15	
cgg cag gtg acg ttc acc aag cgg aag ttc ggg ctg atg aag aag gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gag ctg agc gtg ctc tgt gac tgt gag ata gcc ctc atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc gcc aac cgc ctc ttc cag tat gcc agc acg gac atg gac cgt	192
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg	
50 55 60	
gtg ctg ctg aag tac aca gag tac agc gag ccc cac gag agc cgc acc	240
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac act gac atc ctc gag acg ctg aag cgg agg ggc att ggc ctc gat	288
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp	
85 90 95	
ggg cca gag ctg gag ccg gat gaa ggg cct gag gag cca gga gag aag	336
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys	
100 105 110	
ttt cgg agg ctg gca ggc gaa ggg ggt gat ccg gcc ttg ccc cga ccc	384
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro	
115 120 125	
cgg ctg tat cct gca gct cct gct atg ccc agc cca gat gtg gta tac	432
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr	
130 135 140	
ggg gcc tta ccg cca cca ggc tgt gac ccc agt ggg ctt ggg gaa gca	480
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala	
145 150 155 160	
ctg ccc gcc cag agc cgc cca tct ccc ttc cga cca gca gcc ccc aaa	528
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys	
165 170 175	

gcc ggg ccc cca ggc ctg gtg cac cct ctc ttc tca cca agc cac ctc	576
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu	
180 185 190	
acc agc aag aca cca ccc cca ctg tac ctg ccg acg gaa ggg cgg agg	624
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg	
195 200 205	
tca gac ctg cct ggt ggc ctg gct ggg ccc cga ggg gga cta aac acc	672
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr	
210 215 220	
tcc aga agc ctc tac agt ggc ctg cag aac ccc tgc tcc act gca act	720
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr	
225 230 235 240	
ccc gga ccc cca ctg ggg agc ttc ccc ttc ctc ccc gga ggc ccc cca	768
Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro	
245 250 255	
gtg ggg gcc gaa gcc tgg gcg agg agg gtc ccc caa ccc gcg gcg cct	816
Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro	
260 265 270	
ccc cgc cga ccc ccc cag tca gca tca agt ctg agc gcc tct ctc cgg	864
Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg	
275 280 285	
ccc ccg ggg gcc ccg gcg act ttc cta aga cct tcc cct atc cct tgc	912
Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys	
290 295 300	
tcc tcg ccc ggt ccc tgg cag agc ctc tgc ggc ctg ggc ccg ccc tgc	960
Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys	
305 310 315 320	
gcc ggc tgc cct tgg ccg acg gct ggc ccc ggt agg aga tca ccc ggt	1008
Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly	
325 330 335	
ggc acc agc cca gag cgc tcg cca ggt acg gcg agg gca cgt ggg gac	1056
Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp	
340 345 350	
ccc acc tcc ctc cag gcc tct tca gag aag acc caa cag	1095
Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln	
355 360 365	

<210> 17

<211> 465

<212> PRT

<213> Homo sapiens

<400> 17

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Arg	Gln	Val	Thr	Phe	Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala
			20					25					30		
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe
		35				40						45			
Asn	Ser	Thr	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys
	50				55				60						
Val	Leu	Leu	Lys	Tyr	Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr
65				70					75					80	
Asn	Ser	Asp	Ile	Val	Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys
			85					90					95		
Asp	Ser	Pro	Asp	Pro	Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu
		100						105					110		
Ser	Glu	Asp	Lys	Tyr	Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile
	115						120					125			
Ser	Arg	Gln	Arg	Leu	Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro
	130					135					140				
Val	Ser	Ile	Pro	Val	Ser	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro
145				150						155				160	
Val	Ser	Ser	Leu	Gly	Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser
			165					170					175		
Leu	Gln	Arg	Asn	Ser	Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser
		180						185					190		
Ala	Gly	Asn	Thr	Gly	Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala
	195					200					205				
Gly	Thr	Ser	Ala	Gly	Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly
	210					215					220				
Leu	Leu	Val	Ser	Pro	Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser
225				230						235				240	
Pro	Pro	Pro	Met	Asn	Leu	Gly	Met	Asn	Asn	Arg	Lys	Pro	Asp	Leu	Arg

	245		250		255
Val	Leu	Ile	Pro	Pro	Gly
			Ser	Lys	Asn
			Thr	Met	Pro
			Ser	Val	Asn
			Gln		
	260		265		270
Arg	Ile	Asn	Asn	Ser	Gln
			Ser	Ala	Gln
			Ser	Leu	Ala
			Thr	Pro	Val
			Val		
	275		280		285
Ser	Val	Ala	Thr	Pro	Thr
			Leu	Pro	Gly
			Gln	Gly	Met
			Gly	Gly	Tyr
			Pro		
	290		295		300
Ser	Ala	Ile	Ser	Thr	Thr
			Tyr	Gly	Thr
			Glu	Tyr	Ser
			Leu	Ser	Ser
			Ala		
	305		310		315
			320		
Asp	Leu	Ser	Ser	Leu	Ser
			Gly	Phe	Asn
			Thr	Ala	Ser
			Ala	Leu	His
			Leu		
			325		330
			335		
Gly	Ser	Val	Thr	Gly	Trp
			Gln	Gln	Gln
			His	Leu	His
			Asn	Met	Pro
			Pro		
			340		345
			350		
Ser	Ala	Leu	Ser	Gln	Leu
			Gly	Ala	Cys
			Thr	Ser	Thr
			His	Leu	Ser
			Gln		
			355		360
			365		
Ser	Ser	Asn	Leu	Ser	Leu
			Pro	Ser	Thr
			Gln	Ser	Leu
			Asn	Ile	Lys
			Ser		
			370		375
			380		
Glu	Pro	Val	Ser	Pro	Pro
			Arg	Asp	Arg
			Thr	Thr	Thr
			Pro	Ser	Arg
			Tyr		
			385		390
			395		400
Pro	Gln	His	Thr	Arg	His
			Glu	Ala	Gly
			Arg	Ser	Pro
			Val	Asp	Ser
			Leu		
			405		410
			415		
Ser	Ser	Cys	Ser	Ser	Ser
			Tyr	Asp	Gly
			Ser	Asp	Arg
			Glu	Asp	His
			Arg		
			420		425
			430		
Asn	Glu	Phe	His	Ser	Pro
			Ile	Gly	Leu
			Thr	Arg	Pro
			Ser	Pro	Asp
			Glu		
			435		440
			445		
Arg	Glu	Ser	Pro	Ser	Val
			Lys	Arg	Met
			Arg	Leu	Ser
			Glu	Gly	Trp
			Ala		
			450		455
			460		

Thr

<210> 18

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1398)

<400> 18

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aga cag gtg aca ttt aca aag agg aaa ttt ggg ttg atg aag aag gct	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gag ctg agc gtg ctg tgt gac tgt gag att gcg ctg atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc acc aac aag ctg ttc cag tat gcc agc acc gac atg gac aaa	192
Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
gtg ctt ctc aag tac acg gag tac aac gag ccg cat gag agc cgg aca	240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac tca gac atc gtg gag acg ttg aga aag aag ggc ctt aat ggc tgt	288
Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys	
85 90 95	
gac agc cca gac ccc gat gcg gac gat tcc gta ggt cac agc cct gag	336
Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu	
100 105 110	
tct gag gac aag tac agg aaa att aac gaa gat att gat cta atg atc	384
Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile	
115 120 125	
agc agg caa aga ttg tgt gct gtt cca cct ccc aac ttc gag atg cca	432
Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro	
130 135 140	
gtc tcc atc cca gtg tcc agc cac aac agt ttg gtg tac agc aac cct	480
Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro	
145 150 155 160	
gtc agc tca ctg gga aac ccc aac cta ttg cca ctg gct cac cct tct	528
Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser	
165 170 175	
ctg cag agg aat agt atg tct cct ggt gta aca cat cga cct cca agt	576
Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser	
180 185 190	

gca ggt aac aca ggt ggt ctg atg ggt gga gac ctc acg tct ggt gca	624
Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala	
195 200 205	
ggc acc agt gca ggg aac ggg tat ggc aat ccc cga aac tca cca ggt	672
Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly	
210 215 220	
ctg ctg gtc tca cct ggt aac ttg aac aag aat atg caa gca aaa tct	720
Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser	
225 230 235 240	
cct ccc cca atg aat tta gga atg aat aac cgt aaa cca gat ctc cga	768
Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg	
245 250 255	
gtt ctt att cca cca ggc agc aag aat acg atg cca tca gtg aat caa	816
Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln	
260 265 270	
agg ata aat aac tcc cag tcg gct cag tca ttg gct acc cca gtg gtt	864
Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val	
275 280 285	
tcc gta gca act cct act tta cca gga caa gga atg gga gga tat cca	912
Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro	
290 295 300	
tca gcc att tca aca aca tat ggt acc gag tac tct ctg agt agt gca	960
Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala	
305 310 315 320	
gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct ctt cac ctt	1008
Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu	
325 330 335	
ggt tca gta act ggc tgg caa cag caa cac cta cat aac atg cca cca	1056
Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro	
340 345 350	
tct gcc ctc agt cag ttg gga gct tgc act agc act cat tta tct cag	1104
Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln	
355 360 365	
agt tca aat ctc tcc ctg cct tct act caa agc ctc aac atc aag tca	1152
Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser	
370 375 380	

gaa cct gtt tct cct cct aga gac cgt acc acc acc cct tcg aga tac	1200
Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr	
385 390 395 400	
cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt gac agc ttg	1248
Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu	
405 410 415	
agc agc tgt agc agt tcg tac gac ggg agc gac cga gag gat cac cgg	1296
Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg	
420 425 430	
aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg ccg gac gaa	1344
Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu	
435 440 445	
agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa gga tgg gca	1392
Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala	
450 455 460	
aca	1395
Thr	
465	
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<212> PRT	
<213> Homo sapiens	
<400> 19	
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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys	
85 90 95	
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu	

100	105	110
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe		
115	120	125
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val		
130	135	140
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser		
145	150	155
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro		
165	170	175
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser		
180	185	190
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly		
195	200	205
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly		
210	215	220
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly		
225	230	235
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr		
245	250	255
His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val		
260	265	270
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp		
275	280	285
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr		
290	295	300
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu		
305	310	315
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp		
325	330	335
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser		
340	345	350
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln		
355	360	365
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro		
370	375	380
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro		

385		390		395		400									
Pro	Gln	Gln	Gln	Ser	His	Leu	Val	Pro	Val	Ser	Leu	Ser	Asn	Leu	Ile
		405						410					415		
Pro	Gly	Ser	Pro	Leu	Pro	His	Val	Gly	Ala	Ala	Leu	Thr	Val	Thr	Thr
		420						425					430		
His	Pro	His	Ile	Ser	Ile	Lys	Ser	Glu	Pro	Val	Ser	Pro	Ser	Arg	Glu
		435					440					445			
Arg	Ser	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Val	Phe	Pro	Ala	Ala	Arg	Pro
		450				455					460				
Glu	Pro	Gly	Asp	Gly	Leu	Ser	Ser	Pro	Ala	Gly	Gly	Ser	Tyr	Glu	Thr
465					470					475				480	
Gly	Asp	Arg	Asp	Asp	Gly	Arg	Gly	Asp	Phe	Gly	Pro	Thr	Leu	Gly	Leu
			485					490					495		
Leu	Arg	Pro	Ala	Pro	Glu	Pro	Glu	Ala	Glu	Gly	Ser	Ala	Val	Lys	Arg
		500						505					510		
Met	Arg	Leu	Asp	Thr	Trp	Thr	Leu	Lys							
		515					520								

<210> 20

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1566)

<400> 20

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Met	Gly	Arg	Lys	Lys	Ile	Gln	Ile	Gln	Arg	Ile	Thr	Asp	Glu	Arg	Asn	
1				5					10					15		
cga	cag	gtg	act	ttc	acc	aag	cgg	aag	ttt	ggc	ctg	atg	aag	aag	gcg	96
Arg	Gln	Val	Thr	Phe	Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala	
			20					25					30			
tat	gag	ctg	agc	gtg	cta	tgt	gac	tgc	gag	atc	gca	ctc	atc	atc	ttc	144
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	
		35					40					45				
aac	cac	tcc	aac	aag	ctg	ttc	cag	tac	gcc	agc	acc	gac	atg	gac	aag	192
Asn	His	Ser	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys	

50	55	60	
gtg ctg ctc aag tac acg gag tac aat gag cca cac gag agc cgc acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac gcc gac atc atc gag acc ctg agg aag aag ggc ttc aat ggc tgc			288
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys			
	85	90	95
gac agc ccc gag ccc gac ggg gag gac tgc ctg gaa cag agc ccc ctg			336
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu			
	100	105	110
ctg gag gac aag tac cga cgc gcc agc gag gag ctc gac ggg ctc ttc			384
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe			
	115	120	125
cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt gcc atg cct gtc			432
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val			
	130	135	140
acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc agc aat ccc agc			480
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser			
145	150	155	160
ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc ctc acg gac ccg			528
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro			
	165	170	175
cgg ctc ctg tcc ccc cag cag cca gca cta cag agg aac agt gtg tct			576
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser			
	180	185	190
cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc atg ctg ggg ggt			624
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly			
	195	200	205
gac ctg aac agt gct aac gga gcc tgc ccc agc cct gtt ggg aat ggc			672
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly			
210	215	220	
tac gtc agt gct cgg gct tcc cct ggc ctc ctc cct gtg gcc aat ggc			720
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly			
225	230	235	240
aac agc cta aac aag gtc atc cct gcc aag tct ccg ccc cca cct acc			768
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr			

	245	250	255	
cac agc acc cag ctt gga gcc ccc agc cgc aag ccc gac ctg cga gtc				816
His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val				
	260	265	270	
atc act tcc cag gca gga aag ggg tta atg cat cac ttg act gag gac				864
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp				
	275	280	285	
cat tta gat ctg aac aat gcc cag cgc ctt ggg gtc tcc cag tct act				912
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr				
	290	295	300	
cat tcg ctc acc acc cca gtg gtt tct gtg gca acg ccg agt tta ctc				960
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu				
	305	310	315	320
agc cag ggc ctc ccc ttc tct tcc atg ccc act gcc tac aac aca gat				1008
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp				
	325	330	335	
tac cag ttg acc agt gca gag ctc tcc tcc tta cca gcc ttt agt tca				1056
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser				
	340	345	350	
cct ggg ggg ctg tcg cta ggc aat gtc act gcc tgg caa cag cca cag				1104
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln				
	355	360	365	
cag ccc cag cag ccg cag cag cca cag cct cca cag cag cag cca ccg				1152
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro				
	370	375	380	
cag cca cag cag cca cag cca cag cag cct cag cag ccg caa cag cca				1200
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro				
	385	390	395	400
cct cag caa cag tcc cac ctg gtc cct gta tct ctc agc aac ctc atc				1248
Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile				
	405	410	415	
ccg ggc agc ccc ctg ccc cac gtg ggt gct gcc ctc aca gtc acc acc				1296
Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr				
	420	425	430	
cac ccc cac atc agc atc aag tca gaa ccg gtg tcc cca agc cgt gag				1344
His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu				

435	440	445	
cgc agc cct gcg cct ccc cct cca gct gtg ttc cca gct gcc cgc cct			1392
Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro			
450	455	460	
gag cct ggc gat ggt ctc agc agc cca gcc ggg gga tcc tat gag acg			1440
Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr			
465	470	475	480
gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc aca ctg ggc ctg			1488
Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu			
485	490	495	
ctg cgc cca gcc cca gag cct gag gct gag ggc tca gct gtg aag agg			1536
Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg			
500	505	510	
atg cgg ctt gat acc tgg aca tta aag			1563
Met Arg Leu Asp Thr Trp Thr Leu Lys			
515	520		

<210> 21

<211> 217

<212> PRT

<213> Rattus norvegicus

<400> 21

Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu	
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Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
20 25 30	
Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile	
35 40 45	
Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr	
50 55 60	
Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr	
65 70 75 80	
Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg	
85 90 95	
Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr	
100 105 110	
Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn	

115	120	125
Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala		
130	135	140
Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln		
145	150	155
Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val		160
	165	170
Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr		175
	180	185
Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln		190
	195	200
His Val Trp Ala Leu Glu Leu Lys Gln		205
210	215	

<210> 22

<211> 651

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<223> (1)..(654)

<400> 22

atg agt ctg gtg ggg ggc ttt ccc cac cac ccc gtg gtg cac cat gag	48
Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu	
1 5 10 15	
ggc tac ccg ttc gcc gca gcc gca gcc gcc gct gct gct gcc gcc gcc	96
Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
20 25 30	
agc cgc tgc agt cac gag gag aac ccc tat ttc cac ggc tgg ctt att	144
Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile	
35 40 45	
ggc cac ccg gag atg tcg ccc ccc gac tac agc atg gcc ctg tcc tac	192
Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr	
50 55 60	
agt ccc gag tac gcc agc ggt gcc gcg ggc ctg gac cac tcc cat tat	240
Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr	
65 70 75 80	

ggg gga gtg ccg ccc ggt gcc ggg cct ccc ggc ctg ggg ggg ccg cgc	288
Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg	
85 90 95	
ccg gtg aag cgt cgg ggc acc gcc aac cgc aag gag cgg cgc agg act	336
Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr	
100 105 110	
cag agc atc aac agc gcc ttc gcc gag ctg cgc gag tgc atc ccc aac	384
Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn	
115 120 125	
gtg ccc gcc gac acc aaa ctc tcc aaa atc aag act ctg cgc ctg gcc	432
Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala	
130 135 140	
acc agc tac atc gcc tac ctc atg gat ctg ctg gcc aag gac gac cag	480
Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln	
145 150 155 160	
aac gga gag gcg gag gcc ttc aag gcg gag atc aag aag acc gac gtg	528
Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val	
165 170 175	
aaa gag gag aag agg aag aaa gag ctg aat gaa atc ttg aaa agt aca	576
Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr	
180 185 190	
gtg agc agc aac gac aag aaa acc aaa ggc cgg aca ggc tgg cca cag	624
Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln	
195 200 205	
cac gtc tgg gcc ctg gag ctc aag cag	651
His Val Trp Ala Leu Glu Leu Lys Gln	
210 215	

<210> 23

<211> 215

<212> PRT

<213> Homo sapiens

<400> 23

Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro	
1 5 10 15	
His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala	
20 25 30	

Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
 165 170 175
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
 180 185 190
 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
 195 200 205
 Trp Ala Leu Glu Leu Asn Gln
 210

<210> 24

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 24

atg aac ctc gtg ggc agc tac gca cac cat cac cac cat cac cac ccg 48

Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro

1

5

10

15

cac cct gcg cac ccc atg ctc cac gaa ccc ttc ctc ttc ggt ccg gcc 96

His	Pro	Ala	His	Pro	Met	Leu	His	Glu	Pro	Phe	Leu	Phe	Gly	Pro	Ala		
			20					25					30				
tcg	cgc	tgt	cat	cag	gaa	agg	ccc	tac	ttc	cag	agc	tgg	ctg	ctg	agc	144	
Ser	Arg	Cys	His	Gln	Glu	Arg	Pro	Tyr	Phe	Gln	Ser	Trp	Leu	Leu	Ser		
		35					40					45					
ccg	gct	gac	gct	gcc	ccg	gac	ttc	cct	gcg	ggc	ggg	ccg	ccg	ccc	gcg	192	
Pro	Ala	Asp	Ala	Ala	Pro	Asp	Phe	Pro	Ala	Gly	Gly	Pro	Pro	Pro	Ala		
		50					55				60						
gcc	gct	gca	gcc	gcc	acc	gcc	tat	ggt	cct	gac	gcc	agg	cct	ggg	cag	240	
Ala	Ala	Ala	Ala	Ala	Thr	Ala	Tyr	Gly	Pro	Asp	Ala	Arg	Pro	Gly	Gln		
		65				70				75					80		
agc	ccc	ggg	cgg	ctg	gag	gcg	ctt	ggc	ggc	cgt	ctt	ggc	cgg	cgg	aaa	288	
Ser	Pro	Gly	Arg	Leu	Glu	Ala	Leu	Gly	Gly	Arg	Leu	Gly	Arg	Arg	Lys		
					85				90				95				
ggc	tca	gga	ccc	aag	aag	gag	cgg	aga	cgc	act	gag	agc	att	aac	agc	336	
Gly	Ser	Gly	Pro	Lys	Lys	Glu	Arg	Arg	Arg	Thr	Glu	Ser	Ile	Asn	Ser		
			100				105						110				
gca	ttc	gcg	gag	ttg	cgc	gag	tgc	atc	ccc	aac	gtg	ccg	gcc	gac	acc	384	
Ala	Phe	Ala	Glu	Leu	Arg	Glu	Cys	Ile	Pro	Asn	Val	Pro	Ala	Asp	Thr		
			115				120					125					
aag	ctc	tcc	aag	atc	aag	act	ctg	cgc	cta	gcc	acc	agc	tac	atc	gcc	432	
Lys	Leu	Ser	Lys	Ile	Lys	Thr	Leu	Arg	Leu	Ala	Thr	Ser	Tyr	Ile	Ala		
			130				135					140					
tac	ctg	atg	gac	gtg	ctg	gcc	aag	gat	gca	cag	tct	ggc	gat	ccc	gag	480	
Tyr	Leu	Met	Asp	Val	Leu	Ala	Lys	Asp	Ala	Gln	Ser	Gly	Asp	Pro	Glu		
					145		150			155					160		
gcc	ttc	aag	gct	gaa	ctc	aag	aag	gcg	gat	ggc	ggc	cgt	gag	agc	aag	528	
Ala	Phe	Lys	Ala	Glu	Leu	Lys	Lys	Ala	Asp	Gly	Gly	Arg	Glu	Ser	Lys		
					165				170			175					
cgg	aaa	agg	gag	ctg	cag	cag	cac	gaa	ggt	ttt	cct	cct	gcc	ctg	ggc	576	
Arg	Lys	Arg	Glu	Leu	Gln	Gln	His	Glu	Gly	Phe	Pro	Pro	Ala	Leu	Gly		
			180					185				190					
cca	gtc	gag	aag	agg	att	aaa	gga	cgc	acc	ggc	tgg	ccg	cag	caa	gtc	624	
Pro	Val	Glu	Lys	Arg	Ile	Lys	Gly	Arg	Thr	Gly	Trp	Pro	Gln	Gln	Val		
			195				200					205					
tgg	gcg	ctg	gag	tta	aac	cag										645	

Trp Ala Leu Glu Leu Asn Gln

210

215

<210> 25

<211> 411

<212> PRT

<213> Homo sapiens

<400> 25

Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala

1

5

10

15

Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

20

25

30

Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu

35

40

45

Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu

50

55

60

Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln

65

70

75

80

Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp

85

90

95

Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser

100

105

110

Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro

115

120

125

Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly

130

135

140

Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe

145

150

155

160

Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro

165

170

175

Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln

180

185

190

Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala

195

200

205

Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe

210

215

220

Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu

20										25										30										
gct	atc	tat	cca	cca	tgt	ggg	agg	agg	aaa	atc	atc	tta	tca	gac	gaa	144														
Ala	Ile	Tyr	Pro	Pro	Cys	Gly	Arg	Arg	Lys	Ile	Ile	Leu	Ser	Asp	Glu															
35					40					45																				
ggc	aaa	atg	tat	ggt	agg	aat	gaa	ttg	ata	gcc	aga	tac	atc	aaa	ctc	192														
Gly	Lys	Met	Tyr	Gly	Arg	Asn	Glu	Leu	Ile	Ala	Arg	Tyr	Ile	Lys	Leu															
50					55					60																				
agg	aca	ggc	aag	acg	agg	acc	aga	aaa	cag	gtg	tct	agt	cac	att	cag	240														
Arg	Thr	Gly	Lys	Thr	Arg	Thr	Arg	Lys	Gln	Val	Ser	Ser	His	Ile	Gln															
65					70					75					80															
gtt	ctt	gcc	aga	agg	aaa	tct	cgt	gat	ttt	cat	tcc	aag	cta	aag	gat	288														
Val	Leu	Ala	Arg	Arg	Lys	Ser	Arg	Asp	Phe	His	Ser	Lys	Leu	Lys	Asp															
85					90					95																				
cag	act	gca	aag	gat	aag	gcc	ctg	cag	cac	atg	gcg	gcc	atg	tcc	tca	336														
Gln	Thr	Ala	Lys	Asp	Lys	Ala	Leu	Gln	His	Met	Ala	Ala	Met	Ser	Ser															
100					105					110																				
gcc	cag	atc	gtc	tcg	gcc	act	gcc	att	cat	aac	aag	ctg	ggg	ctg	cct	384														
Ala	Gln	Ile	Val	Ser	Ala	Thr	Ala	Ile	His	Asn	Lys	Leu	Gly	Leu	Pro															
115					120					125																				
ggg	att	cca	cgc	ccg	acc	ttc	cca	ggg	gcg	ccg	ggg	ttc	tgg	ccg	gga	432														
Gly	Ile	Pro	Arg	Pro	Thr	Phe	Pro	Gly	Ala	Pro	Gly	Phe	Trp	Pro	Gly															
130					135					140																				
atg	att	caa	aca	ggg	cag	cca	gga	tcc	tca	caa	gac	gtc	aag	cct	ttt	480														
Met	Ile	Gln	Thr	Gly	Gln	Pro	Gly	Ser	Ser	Gln	Asp	Val	Lys	Pro	Phe															
145					150					155					160															
gtg	cag	cag	gcc	tac	ccc	atc	cag	cca	gcg	gtc	aca	gcc	ccc	att	cca	528														
Val	Gln	Gln	Ala	Tyr	Pro	Ile	Gln	Pro	Ala	Val	Thr	Ala	Pro	Ile	Pro															
165					170					175																				
ggg	ttt	gag	cct	gca	tcg	gcc	cca	gct	ccc	tca	gtc	cct	gcc	tgg	caa	576														
Gly	Phe	Glu	Pro	Ala	Ser	Ala	Pro	Ala	Pro	Ser	Val	Pro	Ala	Trp	Gln															
180					185					190																				
ggt	cgc	tcc	att	ggc	aca	acc	aag	ctt	cgc	ctg	gtg	gaa	ttt	tca	gct	624														
Gly	Arg	Ser	Ile	Gly	Thr	Thr	Lys	Leu	Arg	Leu	Val	Glu	Phe	Ser	Ala															
195					200					205																				
ttt	ctc	gag	cag	cag	cga	gac	cca	gac	tcg	tac	aac	aaa	cac	ctc	ttc	672														
Phe	Leu	Glu	Gln	Gln	Arg	Asp	Pro	Asp	Ser	Tyr	Asn	Lys	His	Leu	Phe															

210	215	220	
gtg cac att ggg cat gcc aac cat tct tac agt gac cca ttg ctt gaa			720
Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu			
225	230	235	240
tca gtg gac att cgt cag att tat gac aaa ttt cct gaa aag aaa ggt			768
Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly			
	245	250	255
ggc tta aag gaa ctg ttt gga aag ggc cct caa aat gcc ttc ttc ctc			816
Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu			
	260	265	270
gta aaa ttc tgg gct gat tta aac tgc aat att caa gat gat gct ggg			864
Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly			
	275	280	285
gct ttt tat ggt gta acc agt cag tac gag agt tct gaa aat atg aca			912
Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr			
	290	295	300
gtc acc tgt tcc acc aaa gtt tgc tcc ttt ggg aag caa gta gta gaa			960
Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu			
305	310	315	320
aaa gta gag acg gag tat gca agg ttt gag aat ggc cga ttt gta tac			1008
Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr			
	325	330	335
cga ata aac cgc tcc cca atg tgt gaa tat atg atc aac ttc atc cac			1056
Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His			
	340	345	350
aag ctc aaa cac tta cca gag aaa tat atg atg aac agt gtt ttg gaa			1104
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu			
	355	360	365
aac ttc aca att tta ttg gtg gta aca aac agg gat aca caa gaa act			1152
Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr			
	370	375	380
cta ctc tgc atg gcc tgt gtg ttt gaa gtt tca aat agt gaa cac gga			1200
Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly			
385	390	395	400
gca caa cat cat att tac agg ctt gta aag gac			1233
Ala Gln His His Ile Tyr Arg Leu Val Lys Asp			

405

410

<210> 27

<211> 427

<212> PRT

<213> Homo sapiens

<400> 27

Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr

1

5

10

15

Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala

20

25

30

Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

35

40

45

Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu

50

55

60

Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu

65

70

75

80

Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln

85

90

95

Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp

100

105

110

Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser

115

120

125

Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala

130

135

140

Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu

145

150

155

160

Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln

165

170

175

Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro

180

185

190

Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln

195

200

205

Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala

210

215

220

Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe

225

230

235

240

Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu	
245	250 255
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly	
260	265 270
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu	
275	280 285
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser	
290	295 300
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile	
305	310 315 320
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu	
325	330 335
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr	
340	345 350
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His	
355	360 365
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu	
370	375 380
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr	
385	390 395 400
Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly	
405	410 415
Ala Gln His His Ile Tyr Arg Leu Val Lys Glu	
420	425

<210> 28

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1284)

<400> 28

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gcc tct ggg ggc agt cag gca ctg gac aag ccc atc gac aat gac gca	96

Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala	
20 25 30	
gag ggc gtg tgg agc ccg gat att gag cag agt ttc cag gag gcc ctc	144
Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu	
35 40 45	
gcc atc tac ccg ccc tgt ggc agg cgc aaa atc atc ctg tgc gac gag	192
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu	
50 55 60	
ggc aag atg tat ggt cgg aac gag ctg att gcc cgc tac atc aag ctc	240
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu	
65 70 75 80	
cgg aca ggg aag acc cgc acc agg aag cag gtc tcc agc cac atc cag	288
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln	
85 90 95	
gtg ctg gct cgt cgc aaa gct cgc gag atc cag gcc aag cta aag gac	336
Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp	
100 105 110	
cag gca gct aag gac aag gcc ctg cag agc atg gct gcc atg tgc tct	384
Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser	
115 120 125	
gca cag atc atc tcc gcc acg gcc ttc cac agt agc atg gcc ctc gcc	432
Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala	
130 135 140	
cgg ggc ccc ggc cgc cca gca gtc tca ggg ttt tgg caa gga gct ttg	480
Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu	
145 150 155 160	
cca ggc caa gcc gga acg tcc cat gat gtg aag cct ttc tct cag caa	528
Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln	
165 170 175	
acc tat gct gtc cag cct ccg ctg cct ctg cca ggg ttt gag tct cct	576
Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro	
180 185 190	
gca ggg ccc gcc cca tgc ccc tct gcg ccc ccg gca ccc cca tgg cag	624
Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln	
195 200 205	
ggc cgc agc gtg gcc agc tcc aag ctc tgg atg ttg gag ttc tct gcc	672

Gly	Arg	Ser	Val	Ala	Ser	Ser	Lys	Leu	Trp	Met	Leu	Glu	Phe	Ser	Ala		
210							215				220						
ttc	ctg	gag	cag	cag	cag	gac	ccg	gac	acg	tac	aac	aag	cac	ctg	ttc	720	
Phe	Leu	Glu	Gln	Gln	Gln	Asp	Pro	Asp	Thr	Tyr	Asn	Lys	His	Leu	Phe		
225						230				235					240		
gtg	cac	att	ggc	cag	tcc	agc	cca	agc	tac	agc	gac	ccc	tac	ctc	gaa	768	
Val	His	Ile	Gly	Gln	Ser	Ser	Pro	Ser	Tyr	Ser	Asp	Pro	Tyr	Leu	Glu		
			245						250					255			
gcc	gtg	gac	atc	cgc	caa	atc	tat	gac	aaa	ttc	ccg	gag	aaa	aag	ggt	816	
Ala	Val	Asp	Ile	Arg	Gln	Ile	Tyr	Asp	Lys	Phe	Pro	Glu	Lys	Lys	Gly		
			260					265						270			
gga	ctc	aag	gat	ctc	ttc	gaa	cgg	gga	ccc	tcc	aat	gcc	ttt	ttt	ctt	864	
Gly	Leu	Lys	Asp	Leu	Phe	Glu	Arg	Gly	Pro	Ser	Asn	Ala	Phe	Phe	Leu		
			275					280						285			
gtg	aag	ttc	tgg	gca	gac	ctc	aac	acc	aac	atc	gag	gat	gaa	ggc	agc	912	
Val	Lys	Phe	Trp	Ala	Asp	Leu	Asn	Thr	Asn	Ile	Glu	Asp	Glu	Gly	Ser		
			290				295				300						
tcc	ttc	tat	ggg	gtc	tcc	agc	cag	tat	gag	agc	ccc	gag	aac	atg	atc	960	
Ser	Phe	Tyr	Gly	Val	Ser	Ser	Gln	Tyr	Glu	Ser	Pro	Glu	Asn	Met	Ile		
305					310				315						320		
atc	acc	tgc	tcc	acg	aag	gtc	tgc	tct	ttc	ggc	aag	cag	gtg	gtg	gag	1008	
Ile	Thr	Cys	Ser	Thr	Lys	Val	Cys	Ser	Phe	Gly	Lys	Gln	Val	Val	Glu		
					325				330					335			
aaa	gtt	gag	aca	gag	tat	gct	cgc	tat	gag	aat	gga	cac	tac	tct	tac	1056	
Lys	Val	Glu	Thr	Glu	Tyr	Ala	Arg	Tyr	Glu	Asn	Gly	His	Tyr	Ser	Tyr		
			340					345						350			
cgc	atc	cac	cgg	tcc	ccg	ctc	tgt	gag	tac	atg	atc	aac	ttc	atc	cac	1104	
Arg	Ile	His	Arg	Ser	Pro	Leu	Cys	Glu	Tyr	Met	Ile	Asn	Phe	Ile	His		
			355				360					365					
aag	ctc	aag	cac	ctc	cct	gag	aag	tac	atg	atg	aac	agc	gtg	ctg	gag	1152	
Lys	Leu	Lys	His	Leu	Pro	Glu	Lys	Tyr	Met	Met	Asn	Ser	Val	Leu	Glu		
			370				375				380						
aac	ttc	acc	atc	ctg	cag	gtg	gtc	acc	aac	aga	gac	aca	cag	gag	acc	1200	
Asn	Phe	Thr	Ile	Leu	Gln	Val	Val	Thr	Asn	Arg	Asp	Thr	Gln	Glu	Thr		
385					390					395					400		
ttg	ctg	tgc	att	gcc	tat	gtc	ttt	gag	gtg	tca	gcc	agt	gag	cac	ggg	1248	

Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
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gct cag cac cac atc tac agg ctg gtg aaa gaa

1281

Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
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<210> 29

<211> 435

<212> PRT

<213> Homo sapiens

<400> 29

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Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala
 35 40 45

Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly
 50 55 60

Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg
 65 70 75 80

Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val
 85 90 95

Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met
 100 105 110

Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser
 115 120 125

Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe
 130 135 140

Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg
 145 150 155 160

Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln
 165 170 175

Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu
 180 185 190

Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala
 195 200 205

Ala	Ala	Ser	Val	Pro	Val	Trp	Gln	Asp	Arg	Thr	Ile	Ala	Ser	Ser	Arg
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Leu	Arg	Leu	Leu	Glu	Tyr	Ser	Ala	Phe	Met	Glu	Val	Gln	Arg	Asp	Pro
225				230						235					240
Asp	Thr	Tyr	Ser	Lys	His	Leu	Phe	Val	His	Ile	Gly	Gln	Thr	Asn	Pro
			245						250					255	
Ala	Phe	Ser	Asp	Pro	Pro	Leu	Glu	Ala	Val	Asp	Val	Arg	Gln	Ile	Tyr
		260						265					270		
Asp	Lys	Phe	Pro	Glu	Lys	Lys	Gly	Gly	Leu	Lys	Glu	Leu	Tyr	Glu	Lys
	275						280					285			
Gly	Pro	Pro	Asn	Ala	Phe	Phe	Leu	Val	Lys	Phe	Trp	Ala	Asp	Leu	Asn
290						295					300				
Ser	Thr	Ile	Gln	Glu	Gly	Pro	Gly	Ala	Phe	Tyr	Gly	Val	Ser	Ser	Gln
305				310						315					320
Tyr	Ser	Ser	Ala	Asp	Ser	Met	Thr	Ile	Ser	Val	Ser	Thr	Lys	Val	Cys
			325						330					335	
Ser	Phe	Gly	Lys	Gln	Val	Val	Glu	Lys	Val	Glu	Thr	Glu	Tyr	Ala	Arg
		340						345					350		
Leu	Glu	Asn	Gly	Arg	Phe	Val	Tyr	Arg	Ile	His	Arg	Ser	Pro	Met	Cys
	355						360						365		
Glu	Tyr	Met	Ile	Asn	Phe	Ile	His	Lys	Leu	Lys	His	Leu	Pro	Glu	Lys
370						375					380				
Tyr	Met	Met	Asn	Ser	Val	Leu	Glu	Asn	Phe	Thr	Ile	Leu	Gln	Val	Val
385				390						395					400
Thr	Ser	Arg	Asp	Ser	Gln	Glu	Thr	Leu	Leu	Val	Ile	Ala	Phe	Val	Phe
			405						410					415	
Glu	Val	Ser	Thr	Ser	Glu	His	Gly	Ala	Gln	His	His	Val	Tyr	Lys	Leu
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Val Lys Asp

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<211> 1305

<212> DNA

<213> Homo sapiens

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<223> (1)..(1305)

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gag gat ggg ccc gag ggc ctg gac aag ggg ctg gac aac gat gcg gag	96
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu	
20 25 30	
ggc gtg tgg agc ccg gac atc gag cag agc ttc cag gag gcc ctg gcc	144
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala	
35 40 45	
atc tac ccg ccc tgc ggc cgg cgg aag atc atc ctg tca gac gag ggc	192
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly	
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aag atg tac ggc cga aat gag ttg att gca cgc tat att aaa ctg agg	240
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg	
65 70 75 80	
acg ggg aag act cgg acg aga aaa cag gtg tcc agc cac ata cag gtt	288
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val	
85 90 95	
cta gct cgg aag aag gtg cgg gag tac cag gtt ggc atc aag gcc atg	336
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met	
100 105 110	
aac ctg gac cag gtc tcc aag gac aaa gcc ctt cag agc atg gcg tcc	384
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser	
115 120 125	
atg tcc tct gcc cag atc gtc tct gcc agt gtc ctg cag aac aag ttc	432
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe	
130 135 140	
agc cca cct tcc cct ctg ccc cag gcc gtc ttc tcc act tcc tcg cgg	480
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg	
145 150 155 160	
ttc tgg agc agc ccc cct ctc ctg gga cag cag cct gga ccc tct cag	528
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln	
165 170 175	
gac atc aag ccc ttt gca cag cca gcc tac ccc atc cag ccg ccc ctg	576
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu	

180	185	190	
ccg ccg acg ctc agc agt tat gag ccc ctg gcc ccg ctc ccc tca gct			624
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala			
195	200	205	
gct gcc tct gtg cct gtg tgg cag gac cgt acc att gcc tcc tcc cgg			672
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg			
210	215	220	
ctg cgg ctc ctg gag tat tca gcc ttc atg gag gtg cag cga gac cct			720
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro			
225	230	235	240
gac acg tac agc aaa cac ctg ttt gtg cac atc ggc cag acg aac ccc			768
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro			
245	250	255	
gcc ttc tca gac cca ccc ctg gag gca gta gat gtg cgc cag atc tat			816
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr			
260	265	270	
gac aaa ttc ccc gag aaa aag gga gga ttg aag gag ctc tat gag aag			864
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys			
275	280	285	
ggg ccc cct aat gcc ttc ttc ctt gtc aag ttc tgg gcc gac ctc aac			912
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn			
290	295	300	
agc acc atc cag gag ggc ccg gga gcc ttc tat ggg gtc agc tct cag			960
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln			
305	310	315	320
tac agc tct gct gat agc atg acc atc agc gtc tcc acc aag gtg tgc			1008
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys			
325	330	335	
tcc ttt ggc aaa cag gtg gta gag aag gtg gag act gag tat gcc agg			1056
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg			
340	345	350	
ctg gag aac ggg cgc ttt gtg tac cgt atc cac cgc tcg ccc atg tgc			1104
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys			
355	360	365	
gag tac atg atc aac ttc atc cac aag ctg aag cac ctg ccc gag aag			1152
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys			

370	375	380	
tac atg atg aac agc gtg ctg gag aac ttc acc atc ctg cag gtg gtc			1200
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val			
385	390	395	400
acg agc cgg gac tcc cag gag acc ttg ctt gtc att gct ttt gtc ttc			1248
Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe			
	405	410	415
gaa gtc tcc acc agt gag cac ggg gcc cag cac cat gtc tac aag ctc			1296
Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu			
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Val Lys Asp			
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly			
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg			
	35	40	45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro			
	50	55	60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu			
	65	70	75
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val			
	85	90	95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro			
	100	105	110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr			
	115	120	125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val			
	130	135	140

Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val
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Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr
				165					170					175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly
			180					185					190		
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg
			195				200					205			
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg
	210					215					220				
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg
225					230					235					240
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp
				245					250					255	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val
			260					265					270		
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala
		275					280					285			
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His
	290					295					300				
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
305					310					315					320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
			325						330				335		
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro
		340						345					350		
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser
		355					360					365			
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
		370				375					380				
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His
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Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg
			405						410				415		
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln
			420				425					430			

Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu
		435					440					445			
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe
		450				455					460				
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser
465					470					475					480
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser
			485						490					495	
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met
			500					505					510		
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys
		515					520					525			
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe
		530				535					540				
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe
545					550					555					560
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr
			565					570						575	
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His
			580					585					590		
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln
		595					600					605			
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile
		610				615					620				
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val
625					630					635					640
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser
			645					650						655	
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg
			660					665					670		
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg
		675					680					685			
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro
		690				695					700				
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile
705					710					715					720

Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	725	730	735	
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	740	745	750	
Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	755	760	765	
Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	770	775	780	
Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	785	790	795	800
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Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	820	825	830	
Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	835	840	845	
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Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	865	870	875	880
Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	885	890	895	
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Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	930	935	940	
Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	945	950	955	960
Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	965	970	975	
Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	980	985	990	
Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	995	1000	1005	

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Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
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Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
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Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085
Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	
50 55 60	

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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu	
65 70 75 80	
gtg gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg	288
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val	
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Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro	
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Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr	
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val	
145 150 155 160	
ctg gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac	528
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr	
165 170 175	
cag ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga	576
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly	
180 185 190	
ccc cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg	624
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg	
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Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg	
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Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg	
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Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp	
245 250 255	

gcc cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg	816
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val	
260 265 270	
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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala	
275 280 285	
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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His	
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Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro	
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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly	
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gac aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc	1056
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro	
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Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser	
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agg ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag	1152
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln	
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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His	
385 390 395 400	
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Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg	
405 410 415	
gct gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag	1296
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln	
420 425 430	
ggc tct gtg gcg gcc ccc gag gag gag gac aca gac ccc cgt cgc ctg	1344
Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu	
435 440 445	

gtg cag ctg ctc cgc cag cac agc agc ccc tgg cag gtg tac ggc ttc	1392
Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe	
450 455 460	
gtg cgg gcc tgc ctg cgc cgg ctg gtg ccc cca ggc ctc tgg ggc tcc	1440
Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser	
465 470 475 480	
agg cac aac gaa cgc cgc ttc ctc agg aac acc aag aag ttc atc tcc	1488
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser	
485 490 495	
ctg ggg aag cat gcc aag ctc tgc ctg cag gag ctg acg tgg aag atg	1536
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met	
500 505 510	
agc gtg cgg gac tgc gct tgg ctg cgc agg agc cca ggg gtt ggc tgt	1584
Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys	
515 520 525	
gtt ccg gcc gca gag cac cgt ctg cgt gag gag atc ctg gcc aag ttc	1632
Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe	
530 535 540	
ctg cac tgg ctg atg agt gtg tac gtc gtc gag ctg ctc agg tct ttc	1680
Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe	
545 550 555 560	
ttt tat gtc acg gag acc acg ttt caa aag aac agg ctc ttt ttc tac	1728
Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr	
565 570 575	
cgg aag agt gtc tgg agc aag ttg caa agc att gga atc aga cag cac	1776
Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His	
580 585 590	
ttg aag agg gtg cag ctg cgg gag ctg tgc gaa gca gag gtc agg cag	1824
Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln	
595 600 605	
cat cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc	1872
His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile	
610 615 620	
ccc aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg	1920
Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val	
625 630 635 640	

gga gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg	1968
Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser	
645 650 655	
agg gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc	2016
Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg	
660 665 670	
ccc ggc ctc ctg ggc gcc tct gtg ctg ggc ctg gac gat atc cac agg	2064
Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg	
675 680 685	
gcc tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct	2112
Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro	
690 695 700	
gag ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc	2160
Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile	
705 710 715 720	
ccc cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag	2208
Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln	
725 730 735	
aac acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat	2256
Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His	
740 745 750	
ggg cac gtc cgc aag gcc ttc aag agc cac gtc tct acc ttg aca gac	2304
Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp	
755 760 765	
ctc cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc	2352
Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser	
770 775 780	
ccg ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag	2400
Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu	
785 790 795 800	
gcc agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac	2448
Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His	
805 810 815	
gcc gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg	2496
Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro	
820 825 830	

cag ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac	2544
Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp	
835 840 845	
atg gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg	2592
Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu	
850 855 860	
cgt ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg	2640
Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala	
865 870 875 880	
aaa acc ttc ctg agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc	2688
Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys	
885 890 895	
gtg gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag	2736
Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu	
900 905 910	
gcc ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc	2784
Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe	
915 920 925	
ccc tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc	2832
Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser	
930 935 940	
gac tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc	2880
Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe	
945 950 955 960	
aac cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg	2928
Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly	
965 970 975	
gtc ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac	2976
Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn	
980 985 990	
agc ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag	3024
Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln	
995 1000 1005	
gcg tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa	3072
Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln	
1010 1015 1020	

gtt tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc	3120		
Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala			
1025	1030	1035	1040
tcc ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tcg ctg	3168		
Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu			
1045	1050	1055	
ggg gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg	3216		
Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp			
1060	1065	1070	
ctg tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc	3264		
Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr			
1075	1080	1085	
tac gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt	3312		
Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser			
1090	1095	1100	
cgg aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac	3360		
Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn			
1105	1110	1115	1120
ccg gca ctg ccc tca gac ttc aag acc atc ctg gac	3396		
Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp			
1125	1130		

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 34

aagagggcag atctatcgga

20

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 35

atggatctcc tgaaggtgct

20

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 36

aagagggcag atctatcgga

20

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 37

ggaagagtga gcggccatca agg

23

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 38

ctgctggaga ggttattcct cg

22

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 39

gccaacacca acctgtccaa gttc

24

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 40

tgcaaaggct ccaggtctga gggc

24

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 41

ctctctctcc tcaggacaa

19

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
 sequence
 <400> 42
 tggagcaaaa cagaatggct gg 22
 <210> 43
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer
 sequence
 <400> 43
 ctgagatgtc tctctctctc ttag 24
 <210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer
 sequence
 <400> 44
 acaatgactg atgagagatg 20
 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer
 sequence
 <400> 45
 cagacctgaa ggagacct 18
 <210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 46

gtcagcgtaa acagttgc

18

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 47

gccagaagc ggatagaagg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 48

ctgtggttca gggctcagtc

20

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 49

cagtggagct ggacaaagcc

20

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 50

tagcgacggt tctggaacca

20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 51

ctgtcatctc actatgggca

20

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 52

ccaagtccga gcaggaattt

20

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 53

aagacgtcaa gccctttgtg

20

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 54

aaaggagcac actttggtgg

20

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 55

agcaagaata cgatgccatc

20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223>Description of Artificial Sequence: artificially synthesized primer sequence

<400> 56

gaaggggtgg tggtacggtc

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 57

tggaatggc tatgtcagtg

20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 58

ctggtaatct gtgttgtagg

20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 59

caagggcctc tccaaacttg

20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 60

gccccagaga cagcattcca

20

<210> 61

<211> 268

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser

1

5

10

15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys

20

25

30

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala

35

40

45

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
100 105 110

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
115 120 125

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
130 135 140

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
145 150 155 160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
165 170 175

Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
180 185 190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
195 200 205

Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
210 215 220

Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
225 230 235 240

Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
245 250 255

Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
260 265

<210> 62

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(807)

<400> 62

atg gcc cag ccc ctg tgc ccg ccg ctc tcc gag tcc tgg atg ctc tct 48
Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser
1 5 10 15

gcg gcc tgg ggc cca act cgg cgg ccg ccg ccc tcc gac aag gac tgc 96
Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys
20 25 30

ggc cgc tcc ctc gtc tgc tcc cca gac tca tgg ggc agc acc cca gcc 144
Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala
35 40 45

gac agc ccc gtg gcg agc ccc gcg cgg cca ggc acc ctc cgg gac ccc 192
Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

cgc gcc ccc tcc gta ggt agg cgc ggc gcg cgc agc agc cgc ctg ggc 240
Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

agc ggg cag agg cag agc gcc agt gag cgg gag aaa ctg cgc atg cgc 288
Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

acg ctg gcc cgc gcc ctg cac gag ctg cgc cgc ttt cta ccg ccg tcc	336
Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser	
100 105 110	
gtg gcg ccc gcg ggc cag agc ctg acc aag atc gag acg ctg cgc ctg	384
Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu	
115 120 125	
gct atc cgc tat atc ggc cac ctg tcg gcc gtg cta ggc ctc agc gag	432
Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu	
130 135 140	
gag agt ctc cag cgc cgg tgc cgg cag cgc ggt gac gcg ggg tcc cct	480
Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro	
145 150 155 160	
cgg ggc tgc ccg ctg tgc ccc gac gac tgc ccc gcg cag atg cag aca	528
Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr	
165 170 175	
cgg acg cag gct gag ggg cag ggg cag ggg cgc ggg ctg ggc ctg gta	576
Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val	
180 185 190	
tcc gcc gtc cgc gcc ggg gcg tcc tgg gga tcc ccg cct gcc tgc ccc	624
Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro	
195 200 205	
gga gcc cga gct gca ccc gag ccg cgc gac ccg cct gcg ctg ttc gcc	672
Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala	
210 215 220	
gag gcg gcg tgc cct gaa ggg cag gcg atg gag cca agc cca ccg tcc	720
Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser	
225 230 235 240	

ccg ctc ctt ccg ggc gac gtg ctg gct ctg ttg gag acc tgg atg ccc 768
 Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
 245 250 255

ctc tcg cct ctg gag tgg ctg cct gag gag ccc aag 804
 Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
 260 265

<210> 63

<211> 215

<212> PRT

<213> Homo sapiens

<400> 63

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
 85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
 100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
 115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
 130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
 145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
 165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
 180 185 190

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205

Thr Trp Ala Pro Glu Pro Arg
 210

<210> 64

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 64

atg ggc agc ccc cgc tcc ggc ctg agc tgc ctg ctg ttg cac ttg ctg 48
 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

gtc ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144

Thr	Gln	His	Val	Arg	Glu	Gln	Ser	Leu	Val	Thr	Asp	Gln	Leu	Ser	Arg	
	35						40					45				
cgc	ctc	atc	cgg	acc	tac	caa	ctc	tac	agc	cgc	acc	agc	ggg	aag	cac	192
Arg	Leu	Ile	Arg	Thr	Tyr	Gln	Leu	Tyr	Ser	Arg	Thr	Ser	Gly	Lys	His	
	50					55					60					
gtg	cag	gtc	ctg	gcc	aac	aag	cgc	atc	aac	gcc	atg	gca	gag	gac	ggc	240
Val	Gln	Val	Leu	Ala	Asn	Lys	Arg	Ile	Asn	Ala	Met	Ala	Glu	Asp	Gly	
	65				70				75						80	
gac	ccc	ttc	gca	aag	ctc	atc	gtg	gag	acg	gac	acc	ttt	gga	agc	aga	288
Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp	Thr	Phe	Gly	Ser	Arg	
				85				90						95		
gtt	cga	gtc	cga	gga	gcc	gag	acg	ggc	ctc	tac	atc	tgc	atg	aac	aag	336
Val	Arg	Val	Arg	Gly	Ala	Glu	Thr	Gly	Leu	Tyr	Ile	Cys	Met	Asn	Lys	
			100					105						110		
aag	ggg	aag	ctg	atc	gcc	aag	agc	aac	ggc	aaa	ggc	aag	gac	tgc	gtc	384
Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	Gly	Lys	Asp	Cys	Val	
	115					120						125				
ttc	acg	gag	att	gtg	ctg	gag	aac	aac	tac	aca	gcg	ctg	cag	aat	gcc	432
Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr	Ala	Leu	Gln	Asn	Ala	
	130					135					140					
aag	tac	gag	ggc	tgg	tac	atg	gcc	ttc	acc	cgc	aag	ggc	cgg	ccc	cgc	480
Lys	Tyr	Glu	Gly	Trp	Tyr	Met	Ala	Phe	Thr	Arg	Lys	Gly	Arg	Pro	Arg	
	145				150					155					160	
aag	ggc	tcc	aag	acg	cgg	cag	cac	cag	cgt	gag	gtc	cac	ttc	atg	aag	528
Lys	Gly	Ser	Lys	Thr	Arg	Gln	His	Gln	Arg	Glu	Val	His	Phe	Met	Lys	
			165					170					175			
cgg	ctg	ccc	cgg	ggc	cac	cac	acc	acc	gag	cag	agc	ctg	cgc	ttc	gag	576

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180 185 190

ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg 624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195 200 205

act tgg gcc ccg gaa ccc cga 645
Thr Trp Ala Pro Glu Pro Arg
210 215

<210> 65

<211> 212

<212> PRT

<213> Homo sapiens

<400> 65

Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
1 5 10 15

Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
20 25 30

Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg
35 40 45

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
50 55 60

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
65 70 75 80

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
85 90 95

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
100 105 110

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
 115 120 125

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
 130 135 140

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
 145 150 155 160

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
 165 170 175

Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

Arg Ala His Trp
 210

<210> 66

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(639)

<400> 66

atg gat tat ttg ctc atg att ttc tct ctg ctg ttt gtg gct tgc caa 48
 Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
 1 5 10 15

gga gct cca gaa aca gca gtc tta ggc gct gag ctc agc gcg gtg ggt 96
 Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
 20 25 30

gag aac ggc ggg gag aaa ccc act ccc agt cca ccc tgg cgg ctc cgc	144
Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg	
35 40 45	
cgg tcc aag cgc tgc tcc tgc tgc tcc ctg atg gat aaa gag tgt gtc	192
Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val	
50 55 60	
tac ttc tgc cac ctg gac atc att tgg gtc aac act ccc gag cac gtt	240
Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val	
65 70 75 80	
gtt ccg tat gga ctt gga agc cct agg tcc aag aga gcc ttg gag aat	288
Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn	
85 90 95	
tta ctt ccc aca aag gca aca gac cgt gag aat aga tgc caa tgt gct	336
Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala	
100 105 110	
agc caa aaa gac aag aag tgc tgg aat ttt tgc caa gca gga aaa gaa	384
Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu	
115 120 125	
ctc agg gct gaa gac att atg gag aaa gac tgg aat aat cat aag aaa	432
Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys	
130 135 140	
gga aaa gac tgt tcc aag ctt ggg aaa aag tgt att tat cag cag tta	480
Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu	
145 150 155 160	
gtg aga gga aga aaa atc aga aga agt tca gag gaa cac cta aga caa	528
Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln	
165 170 175	

acc agg tcg gag acc atg aga aac agc gtc aaa tca tct ttt cat gat 576
 Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

ccc aag ctg aaa ggc aag ccc tcc aga gag cgt tat gtg acc cac aac 624
 Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

cga gca cat tgg 636
 Arg Ala His Trp
 210

<210> 67

<211> 143

<212> PRT

<213> Homo sapiens

<400> 67

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
 85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 68

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(432)

<400> 68

atg cag cac cga ggc ttc ctc ctc ctc acc ctc ctc gcc ctg ctg gcg 48
 Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

ctc acc tcc gcg gtc gcc aaa aag aaa gat aag gtg aag aag ggc ggc 96
 Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

ccg ggg agc gag tgc gct gag tgg gcc tgg ggg ccc tgc acc ccc agc 144
 Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

agc aag gat tgc ggc gtg ggt ttc cgc gag ggc acc tgc ggg gcc cag 192
 Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

acc cag cgc atc cgg tgc agg gtg ccc tgc aac tgg aag aag gag ttt 240
 Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

gga gcc gac tgc aag tac aag ttt gag aac tgg ggt gcg tgt gat ggg 288
 Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly

85	90	95	
ggc aca ggc acc aaa gtc cgc caa ggc acc ctg aag aag gcg cgc tac			336
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr			
100	105	110	
aat gct cag tgc cag gag acc atc cgc gtc acc aag ccc tgc acc ccc			384
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro			
115	120	125	
aag acc aaa gca aag gcc aaa gcc aag aaa ggg aag gga aag gac			429
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp			
130	135	140	
<210> 69			
<211> 408			
<212> PRT			
<213> Homo sapiens			
<400> 69			
Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val			
1	5	10	15
Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys			
20	25	30	
Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly			
35	40	45	
Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met			
50	55	60	
Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro			
65	70	75	80
Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu			
85	90	95	

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser		
100	105	110
Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn		
115	120	125
Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu		
130	135	140
Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu		
145	150	155 160
Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His		
165	170	175
Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro		
180	185	190
Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn		
195	200	205
Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp		
210	215	220
Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His		
225	230	235 240
Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg		
245	250	255
Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu		
260	265	270
Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg		
275	280	285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
 405

<210> 70

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1227)

<400> 70

atg att cct ggt aac cga atg ctg atg gtc gtt tta tta tgc caa gtc 48
 Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
 1 5 10 15

ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag 96

Leu	Leu	Gly	Gly	Ala	Ser	His	Ala	Ser	Leu	Ile	Pro	Glu	Thr	Gly	Lys	
				20				25						30		
aaa	aaa	gtc	gcc	gag	att	cag	ggc	cac	gcg	gga	gga	cgc	cgc	tca	ggg	144
Lys	Lys	Val	Ala	Glu	Ile	Gln	Gly	His	Ala	Gly	Gly	Arg	Arg	Ser	Gly	
		35					40					45				
cag	agc	cat	gag	ctc	ctg	cgg	gac	ttc	gag	gcg	aca	ctt	ctg	cag	atg	192
Gln	Ser	His	Glu	Leu	Leu	Arg	Asp	Phe	Glu	Ala	Thr	Leu	Leu	Gln	Met	
		50				55					60					
ttt	ggg	ctg	cgc	cgc	cgc	ccg	cag	cct	agc	aag	agt	gcc	gtc	att	ccg	240
Phe	Gly	Leu	Arg	Arg	Arg	Pro	Gln	Pro	Ser	Lys	Ser	Ala	Val	Ile	Pro	
		65				70				75					80	
gac	tac	atg	cgg	gat	ctt	tac	cgg	ctt	cag	tct	ggg	gag	gag	gag	gaa	288
Asp	Tyr	Met	Arg	Asp	Leu	Tyr	Arg	Leu	Gln	Ser	Gly	Glu	Glu	Glu	Glu	
				85					90					95		
gag	cag	atc	cac	agc	act	ggt	ctt	gag	tat	cct	gag	cgc	ccg	gcc	agc	336
Glu	Gln	Ile	His	Ser	Thr	Gly	Leu	Glu	Tyr	Pro	Glu	Arg	Pro	Ala	Ser	
			100					105						110		
cgg	gcc	aac	acc	gtg	agg	agc	ttc	cac	cac	gaa	gaa	cat	ctg	gag	aac	384
Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	His	His	Glu	Glu	His	Leu	Glu	Asn	
		115					120					125				
atc	cca	ggg	acc	agt	gaa	aac	tct	gct	ttt	cgt	ttc	ctc	ttt	aac	ctc	432
Ile	Pro	Gly	Thr	Ser	Glu	Asn	Ser	Ala	Phe	Arg	Phe	Leu	Phe	Asn	Leu	
		130				135					140					
agc	agc	atc	cct	gag	aac	gag	gcg	atc	tcc	tct	gca	gag	ctt	cgg	ctc	480
Ser	Ser	Ile	Pro	Glu	Asn	Glu	Ala	Ile	Ser	Ser	Ala	Glu	Leu	Arg	Leu	
		145			150				155					160		
ttc	cgg	gag	cag	gtg	gac	cag	ggc	cct	gat	tgg	gaa	agg	ggc	ttc	cac	528

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His	
165	170 175
cg t ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct	576
Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro	
180	185 190
ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat	624
Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn	
195	200 205
gtg aca cgg tgg gaa act ttt gat gtg agc cct gcg gtc ctt cgc tgg	672
Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp	
210	215 220
acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac	720
Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His	
225	230 235 240
ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga	768
Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg	
245	250 255
tcg tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg	816
Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu	
260	265 270
gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg	864
Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg	
275	280 285
agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag	912
Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys	
290	295 300
aat aag aac tgc cgg cgc cac tcg ctc tat gtg gac ttc agc gat gtg	960

Asn	Lys	Asn	Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val
305						310				315					320

ggc	tgg	aat	gac	tgg	att	gtg	gcc	cca	cca	ggc	tac	cag	gcc	ttc	tac	1008
Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	
				325					330					335		

tgc	cat	ggg	gac	tgc	ccc	ttt	cca	ctg	gct	gac	cac	ctc	aac	tca	acc	1056
Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	
				340				345						350		

aac	cat	gcc	att	gtg	cag	acc	ctg	gtc	aat	tct	gtc	aat	tcc	agt	atc	1104
Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	
		355					360					365				

ccc	aaa	gcc	tgt	tgt	gtg	ccc	act	gaa	ctg	agt	gcc	atc	tcc	atg	ctg	1152
Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	
		370				375					380					

tac	ctg	gat	gag	tat	gat	aag	gtg	gta	ctg	aaa	aat	tat	cag	gag	atg	1200
Tyr	Leu	Asp	Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	
385					390					395				400		

gta	gta	gag	gga	tgt	ggg	tgc	cgc	1224
Val	Val	Glu	Gly	Cys	Gly	Cys	Arg	
				405				

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 71

gccccgcgctc caactgctct gatg

24

<210> 72

<211> 24

<212> DNA

<213> Artificial Sequence
<400> 72
tgcctacggt ggtgcgccct ctgc

24

<210> 73
<211> 22
<212> DNA
<213> Artificial Sequence
<400> 73
gaagcgcaac agggccatca cg

22

<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence
<400> 74
ccacgtcacg caggtcccgt tc

22

<210> 75
<211> 22
<212> DNA
<213> Artificial Sequence
<400> 75
gatcctgttc tctgcctctg ga

22

<210> 76
<211> 22
<212> DNA
<213> Artificial Sequence
<400> 76
tcatccactt tgtccaccg ag

22

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<400> 77

ttcctcgtct tggccttttg g

21

<210> 78

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 78

gctggatctt cgtaggctcc g

21

<210> 79

<211> 19

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<213> Artificial Sequence

<400> 79

ggcaagctga ccctgaagt

19

<210> 80

<211> 19

<212> DNA

<213> Artificial Sequence

<400> 80

gggtgctcag gtagtggtt

19